RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEM
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/516,088_

Source: _PCT/10_

Date Processed by STIC: _12/7/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):** U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	**SUGGESTED CORRECTION**	**SERIAL NUMBER:** _10/516,088_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

```
        RAW SEQUENCE LISTING              DATE: 12/07/2004
        PATENT APPLICATION:  US/10/516,088   TIME: 11:03:13

        Input Set : A:\pto.1m.txt
        Output Set: N:\CRF4\12072004\J516088.raw        see item 2 on Error
                                                          Summary Sheet

      3 <110> APPLICANT: BRANCIA, FRANCESCO LORENZO
      6 <120> TITLE OF INVENTION: SELECTIVE BINDING AND ANALYSIS OF MACROMOLECULES   pp 1-2
      9 <130> FILE REFERENCE: 12687/P70284US0
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/516,088
C--> 12 <141> CURRENT FILING DATE: 2004-11-30                          Does Not Comply
     14 <150> PRIOR APPLICATION NUMBER: GB0212522.7              Corrected Diskette Needed
     15 <151> PRIOR FILING DATE: 2002-05-31
E--> 16 <160> NUMBER OF SEQ ID:(3)4 (see below)
     17 <170> SOFTWARE: PatentIn version 3.1


ERRORED SEQUENCES
                                                            give source of genetic
                                                                       material
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 7
     21 <212> TYPE: PRT
     22 <213> ORGANISM: Artificial Sequence
W--> 23 <220> FEATURE:
     24 <223> OTHER INFORMATION: Lysine terminal standard peptide (AFLDASK)    (see item 11
W--> 25 <400> SEQUENCE: 1                                                       on Error
     27 Ala Phe Leu Asp Ala Ser Lys                                             Summary
E--> 28 1        5   5 <- misaligned numbers-see                               Sheet )
     30 <210> SEQ ID NO: 2                     item 3 on
     31 <211> LENGTH: 7                      Error Summary Sheet
     32 <212> TYPE: PRT
     33 <213> ORGANISM: Artificial Sequence
W--> 34 <220> FEATURE:
     35 <223> OTHER INFORMATION: Homoarginine terminal standard peptide made by guanidination
of the
     36        terminal Lys and identified in the specification as AFLDASK* <- please explain
W--> 37 <400> SEQUENCE: 2                                                      further - give
     39 Ala Phe Leu Asp Ala Ser Arg                                            source of genetic
E--> 41 1        5   5 <- misaligned                                           material
     43 <210> SEQ ID NO: 3
     44 <211> LENGTH: 7
     45 <212> TYPE: PRT
     46 <213> ORGANISM: Artificial Sequence
W--> 47 <220> FEATURE:
     48 <223> OTHER INFORMATION: Arginine terminal standard peptide (AFLDASR)
W--> 49 <400> SEQUENCE: 3
     51 Ala Phe Leu Asp Ala Ser Arg
E--> 52 1        5   5 <- misaligned
     54 <210> SEQ ID NO: 4     last sequence in submitted file
     55 <211> LENGTH: 9
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/516,088**

DATE: 12/07/2004
TIME: 11:03:13

Input Set : **A:\pto.lm.txt**
Output Set: **N:\CRF4\12072004\J516088.raw**

```
        56 <212> TYPE: PRT        ( Interleukin )  invalid response — see item 10 on Error Summary Sheet
        57 <213> ORGANISM: Interleukin
W--> 58 <220> FEATURE:
        59 <223> OTHER INFORMATION: Synthetic peptide standard (SIGMA)
W--> 60 <400> SEQUENCE: 4
        62 Val Gln Gly Glu Glu Ser Asn Asp Lys
·E--> 63 1        5        5
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/516,088**

DATE: 12/07/2004
TIME: 11:03:14

Input Set : **A:\pto.1m.txt**
Output Set: **N:\CRF4\12072004\J516088.raw**

```
L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:283 W: Missing Blank Line separator, <160> field identifier
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:28 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:34 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:47 M:283 W: Missing Blank Line separator, <220> field identifier
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:58 M:283 W: Missing Blank Line separator, <220> field identifier
L:60 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (3) Counted (4)
```